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REPLACEMENT SHEET

Fig. 1A

Restriction map of plasmid ms23

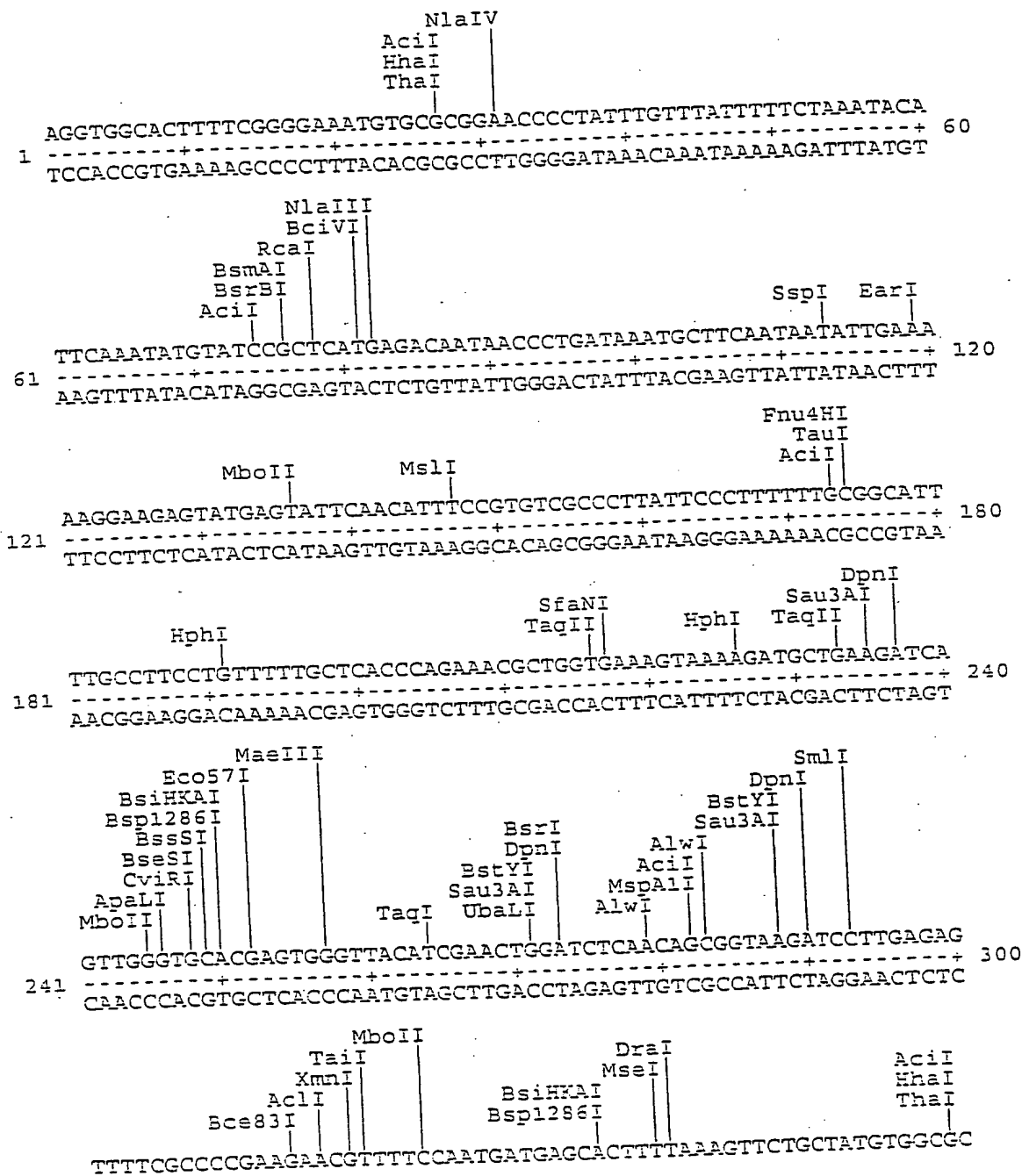


Fig. 1A (cont.)

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301
AAAAGCGGGCTTCTTGCAAAAGGTTACTACTCGTGAAAATTTCAAGACGATACACCGCG 360

HgaI
TaqII
NciI
ScrFI
MspI
BcgI
BscGI
BsaHI
AcII
Fnu4HI
TauI
BsiEI
BseMII
DdeI
BcgI

GGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTGCGCCGATACACTATTCTCA
361
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
CCATAATAGGGCATAACTGCGGCCCGTTCTCGTTGAGCCAGCGCGTATGTGATAAGAGT

RsaI
ScaI
MaeIII
Tsp45I
BsrI
HphI
TatI
SfaNI
BccI
NlaIII
Bst4CI
FokI

GAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGT
421
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
CTTACTGAACCAACTCATGAGTGGTCAGTGTCTTTTCGTAGAATGCCTACCGTACTGTCA

CviJI
HaeIII
TspRI
EaeI
Fnu4HI
GdiII
TauI
AcII
BtsI
Tsp509I
BbvI
CviRI
BtsI
TspRI
Fnu4HI
TseI
MslI
NlaIII
CjePI

AAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAAACTGCGGCCAACTTACTTCT
481
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
TTCTCTTAATACGTCACGACGGTATTGGTACTCACTATTGTGACGCCGTTGAATGAAGA

AvaII
Sau96I
CjePI
BsiEI
PvuI
DpnI
Sau3AI
MnlI
AluI
TaqII
CviJI
AcII
CviRI
NlaIII
Sau3AI
DpnI
MaeIII
AlwI

GACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGT
541
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
CTGTTGCTAGCCTCCTGGCTTCCTCGATTGGCGAAAAACGTGTTGTACCCCTAGTACA

AceIII
DpnI
Sau3AI
MspI
BsaWI
NlaIV
AluI
CviJI
CviJI
SfaNI
MaeIII
Tsp45I

AACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGA
601
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
TTGAGCGGAAGTACCAACCCTTGGCCTCGACTTACTTCGGTATGGTTGTCTGCTCGCACT

HhaI
FspI
Tail
MslI
SfcI
BsrDI
AclI
MseI
BsrI

CACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAAGTGGCGAACTACT
661
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
GTGGTGCTACGACATCGTTACCGTTGTTGCAACGCGTTTGATAATTGACCGCTTGATGA

MseI

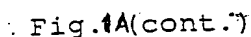


Fig. 1A (cont.)

Restriction sites (enzymes) indicated above the sequence:

RcaI, NlaIII, MseI, Tail, CjeI, Bsp24I, UbaLI, BsaMII, DdeI, TspRI, SimI, BscGI

Sequence (1081-1140):

TAATCTCATGACCAAAATCCCTTAACGTGAGTTCGTTCCACTGAGCGTCAGACCCCGT
-----+-----+-----+-----+-----+-----+-----+-----+
ATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCA

DpnI
 BstYI
 Sau3AI
 MboII
 DpnI
 Sau3AI
 CjeI
 CjePI
 Bsp24I
 DpnI
 BstYI
 Sau3AI
 AlwI
 SmlI
 AlwI
 DpnI
 Tth111II
 Sca83I
 KhaI
 ThaI
 BbvI
 CviRI
 Cac8I
 Fnu4HI
 TseI
 MwoI

AGAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCA
 TCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGT

1141 1200

[illegible]

Eco57I MaeIII BsrI CviJI CjePI FhaI Bsp24I CjePI CjeI BceFI Bst4CI BfaI
 TTTTCCGAAGGTTAACTGGCTTCAGCAGAGCGCAGATACCAATACTGTCTCTTAGTGTA
 1261 +-----+-----+-----+-----+-----+-----+-----+-----+
 AAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGCAAGATCACAT 1320

CjaI CviJI
CjePI HaeI
Bsp24I HaeIII
CviJI BslI SfiI AclI MnlI

GCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCT 1360
-----+-----+-----+-----+
CGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGA

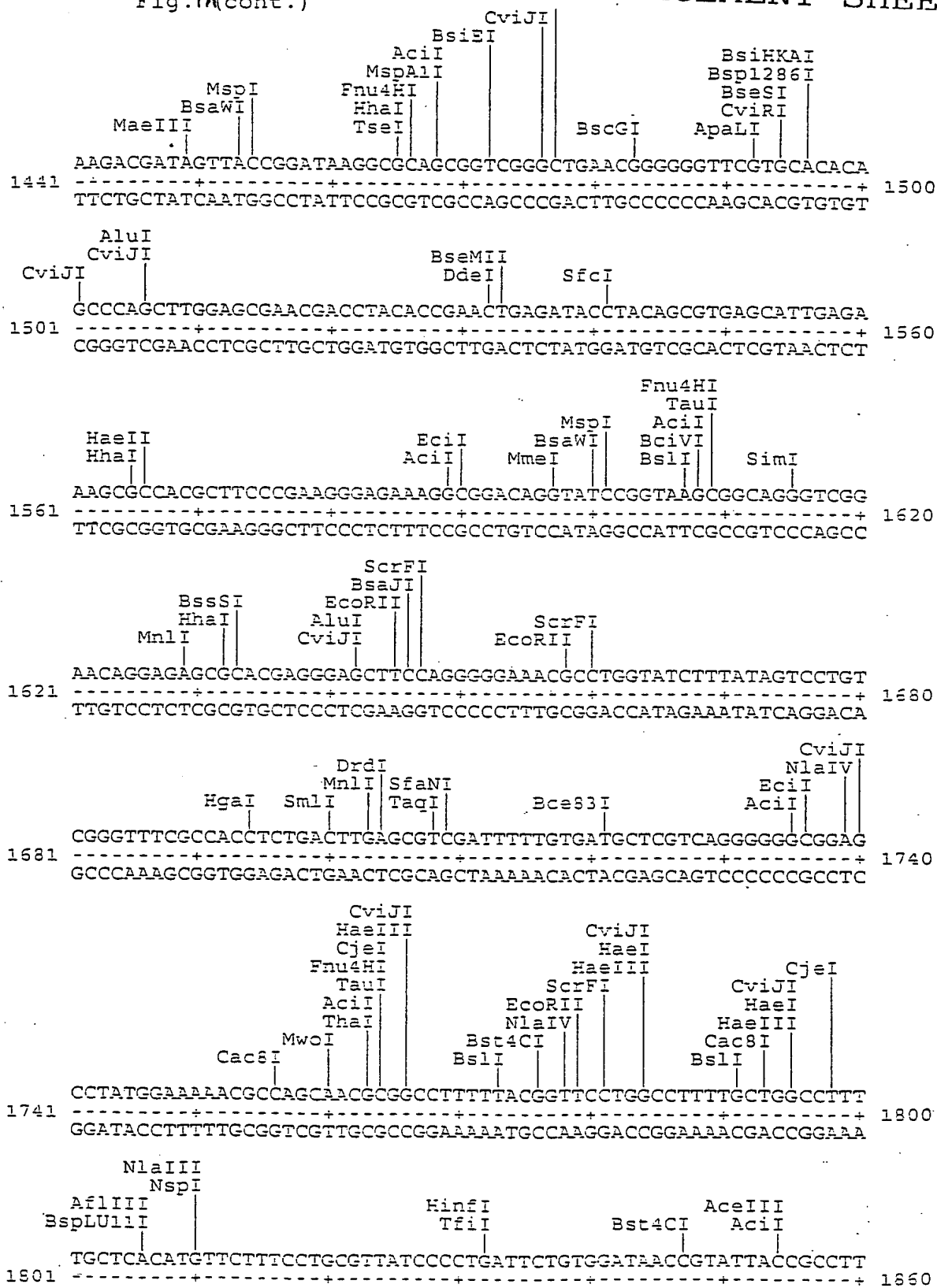
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END



Fig.1A(cont.)

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Fig.1A(cont.)

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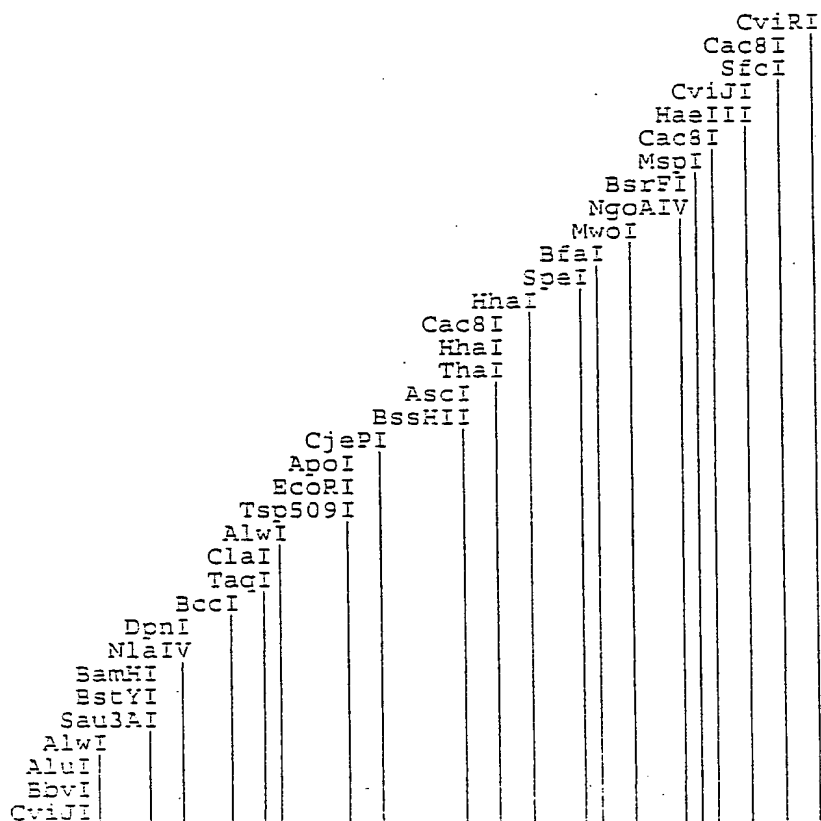
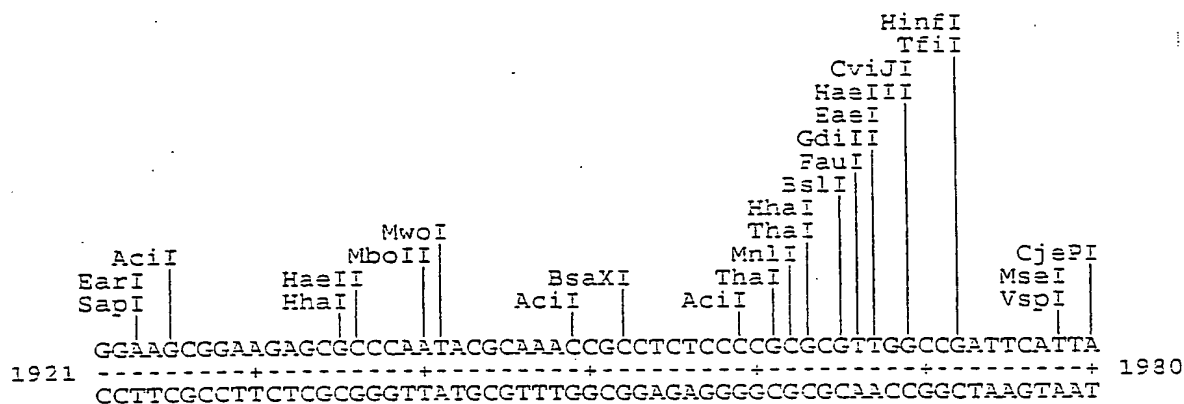
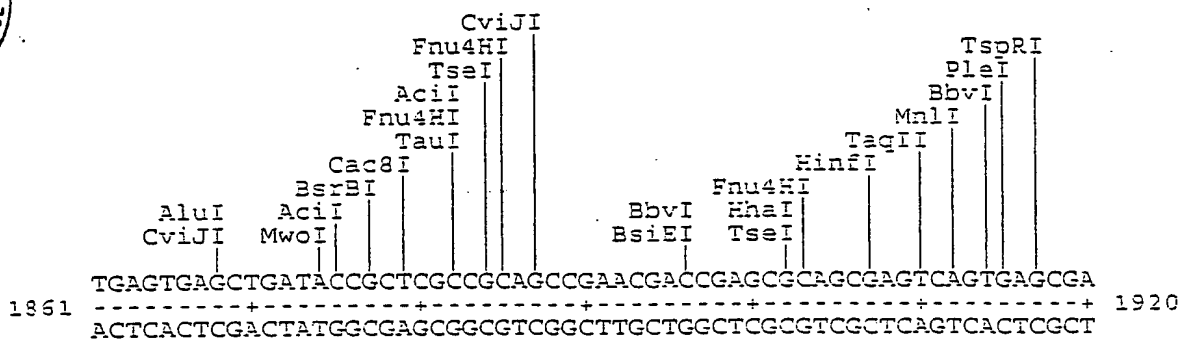




Fig.1A(cont.)

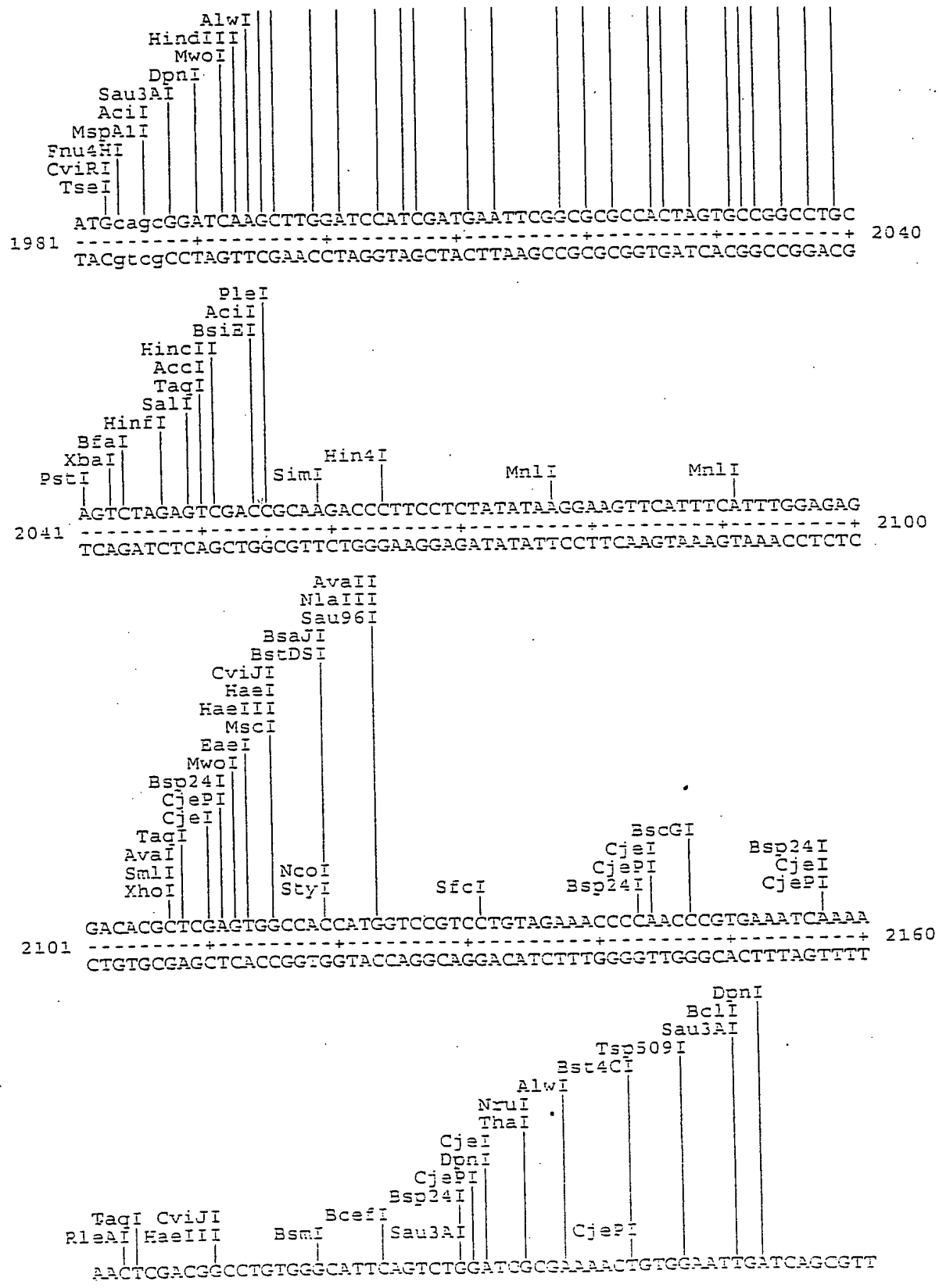


Fig. 1A(cont.)

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[illegible]

Fig.1A(cont.)

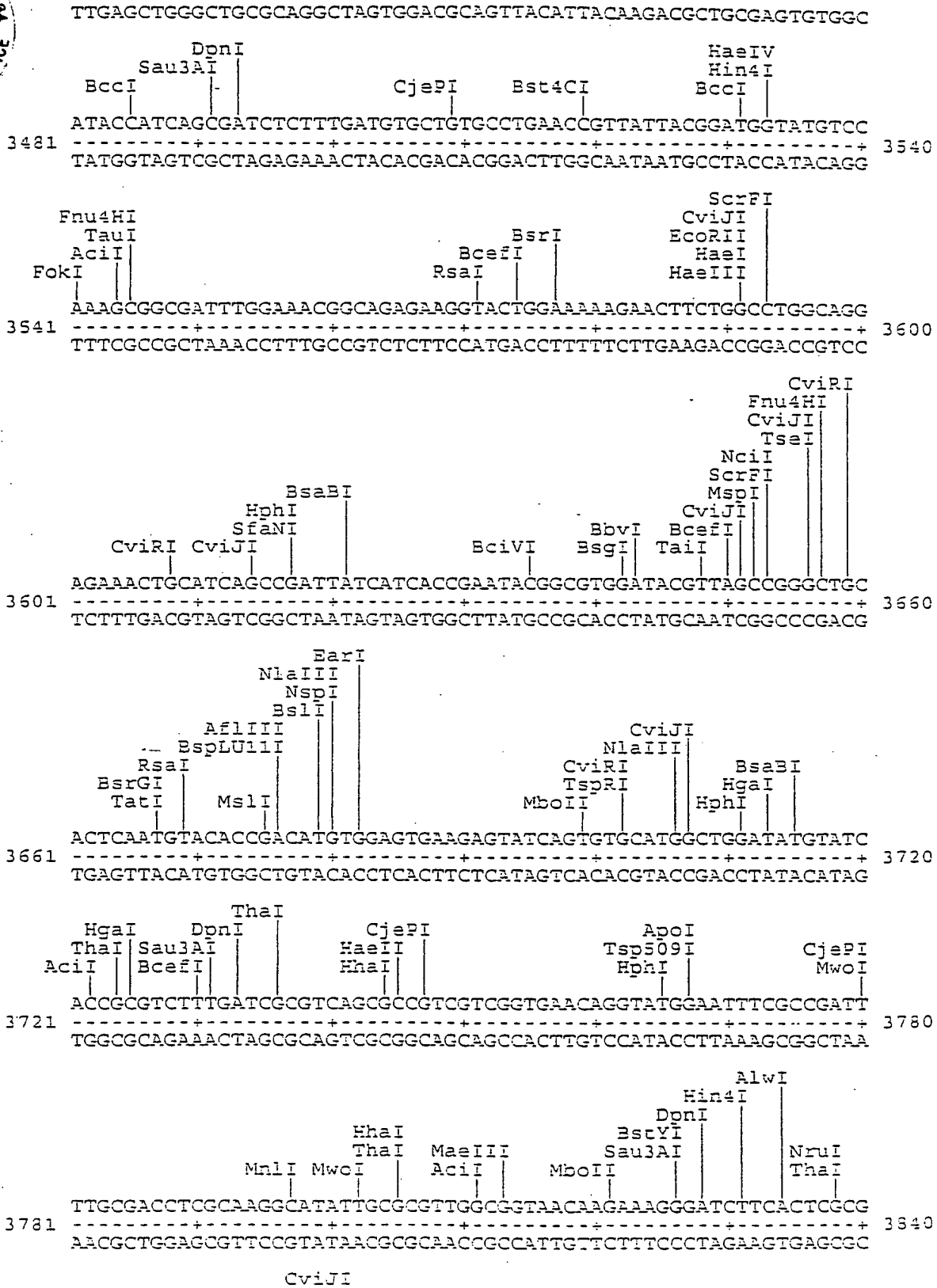
PAGE 4
 CviJI
 HaeIII
 NlaIV
 Sau96I
 BsrI
 RsaI
 Bst4CI
 MnlI
 EarI
 SfaNI
 MseI
 VspI
 ACCACGCATTAAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACG 3120
 TGGTGCCTAATTACCTGACCTAACCCCGGTTGAGGATGGCATGGAGCGTAATGGGAATGC
 BfiI
 BbvI
 Fnu4HI
 TseI
 MboII
 Eco57I
 BsrI
 NlaIII
 MslI
 HphI
 CTGAAGAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAACTGCTG 3180
 GACTTCTCTACGAGCTGACCCGTCTACTTGTACCGTAGCACCCTAACTACTTTGACGAC
 NspV
 TaqI
 Cac8I
 CviJI
 BcgI
 MseI
 CviJI
 BcgI
 MnlI
 FauI
 AciI
 CTGTCGGCTTTTAACCTCTCTTTAGGCATTGGTTTTCGAAGCGGGCAACAAGCCGAAAGAAC 3240
 GACAGCCGAAATTGGAGAGAAATCCGTAACCAAAGCTTCGCCCGTTGTTCCGGCTTTCTTG
 MnlI
 EarI
 RsaI
 BsrGI
 Bst4CI
 TacI
 BscGI
 MboII
 HincII
 BseMII
 DdeI
 Cac8I
 HhaI
 AceIII
 MseI
 TGTACAGCGAAGAGGCAGTCAACGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAG 3300
 ACATGTCGCTTCTCCGTCAGTTGCCCTTTGAGTCGTTCCGCTGAATGTCCGCTAATTTG
 MaeIII
 Tsp45I
 HhaI
 ThaI
 AluI
 CviJI
 MwoI
 CjeI
 BslI
 TaqII
 HphI
 CjeI
 BciVI
 MspI
 BsaWI
 AGCTGATAGCGCGTGACAAAAACCACCCAAGCGTGGTGATGTGGAGTATTGCCAACGAAC 3360
 TCGACTATCGCGCACTGTTTTTGGTGGGTTCGCACCACTACACCTCATAACGGTTGCTTG
 BscGI
 BsiHKAI
 Bsp1286I
 BseSI
 CviRI
 BscGI
 AciI
 ApaLI
 SspI
 HhaI
 ThaI
 MwoI
 BsrI
 BciI
 TspRI
 AciI
 AflIII
 MluI
 ThaI
 CGGATAACCGTCCGCAAGGTGCACGGGAATATTTTCGCCCACTGGCGGAAGCAACGCGTA 3420
 GCCTATGGGCAGGCGTTCCACGTGCCCTTATAAAGCGCGGTGACCGCCTTCGTTGCGCAT
 DpnI
 HgaI
 Sau3AI
 HgaI
 HphI
 ThaI
 SimI
 TagI
 HgaI
 AflIII
 MluI
 AarI
 BspMI
 HgaI
 CjeI
 AACTCGACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCG 3480



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Fig.1A(cont.)

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Fnu4HI
 TauI
 CviRI
 MwoI
 NlaIII
 BsrI
 BspGI
 BcgI
 Fnu4HI
 TseI
 BbvI
 AciI
 BsiEI
 AciI
 BsiEI
 ACCGCAAACCGAAGTCGGCGGCTTTTCTGCTGCAAAAACGCTGGACTGGCATGAACTTCG
 3841
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 3900
 BsiI
 BcgI
 Fnu4HI
 HphI
 MnlI
 TseI
 AciI
 BbvI
 HinfI
 TfiI
 Tth1111I
 BcgI
 EcoRII
 ScrFI
 HhaI
 BccI
 GTGAAAAACCGCAGCAGGGAGGCAAAACAATGAATCAACAACCTCTCCTGGCGCACCATCGT
 3901
 CACTTTTGGCGTCGTCCTCCGTTTGTACTTAGTTGTTGAGAGGACCGCGTGGTAGCA
 3960
 Tsp509I
 NlaIII
 RcaI
 DpnI
 BclI
 Sau3AI
 KpnI
 NlaIV
 RsaI
 BaniI
 NciI
 ScrFI
 SmaI
 MspI
 NciI
 ScrFI
 AvaI
 BsaJI
 BaniI
 BsiHKA
 Bsp1286I
 SacI
 AluI
 CviJI
 Tsp509I
 AvaI
 BsaJI
 CviJI
 SfcI
 BcgI
 MnlI
 CGCTACAGCCTCGGGAATTGCTACCGAGCTccccgggtacctgatcatgagtaattagctC
 3961
 GCGATGTCGGAGCCCTTAACGATGGCTCGAgggcccatggactagtagtactcattaatcgag
 4020
 BsiEI
 PvuI
 DpnI
 ApoI
 Tsp509I
 Sau3AI
 Tth1111I
 AflIII
 SmlI
 MseI
 HinfI
 TfiI
 BsiI
 BsrFI
 MspI
 GAATTTCCCGGATCGTTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGC
 4021
 CTTAAAGGGGCTAGCAAGTTTGTAAACCGTTATTTCAAAGAATTCTAATTAGGACAACG
 4080
 AflIII
 BspLUIII
 MseI
 Tsp509I
 NlaIII
 NspI
 MseI
 Tail
 Tsp509I
 BsaBI
 Tsp509I
 Tsp509I
 MwoI
 CGGTCITGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAA
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 4140



REPLACEMENT SHEET

pGPTV-GUS-kan

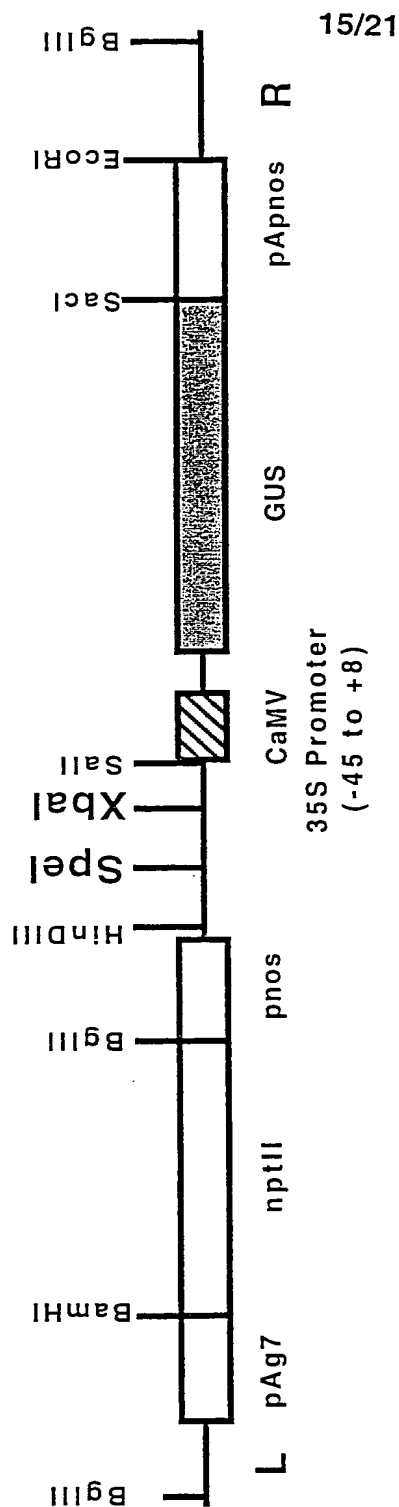


Fig. 3

REPLACEMENT SHEET

Fig. 4

